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1 **Title**

2 Dynamic Energy Budget Models in ecological risk assessment:
3 From principles to applications

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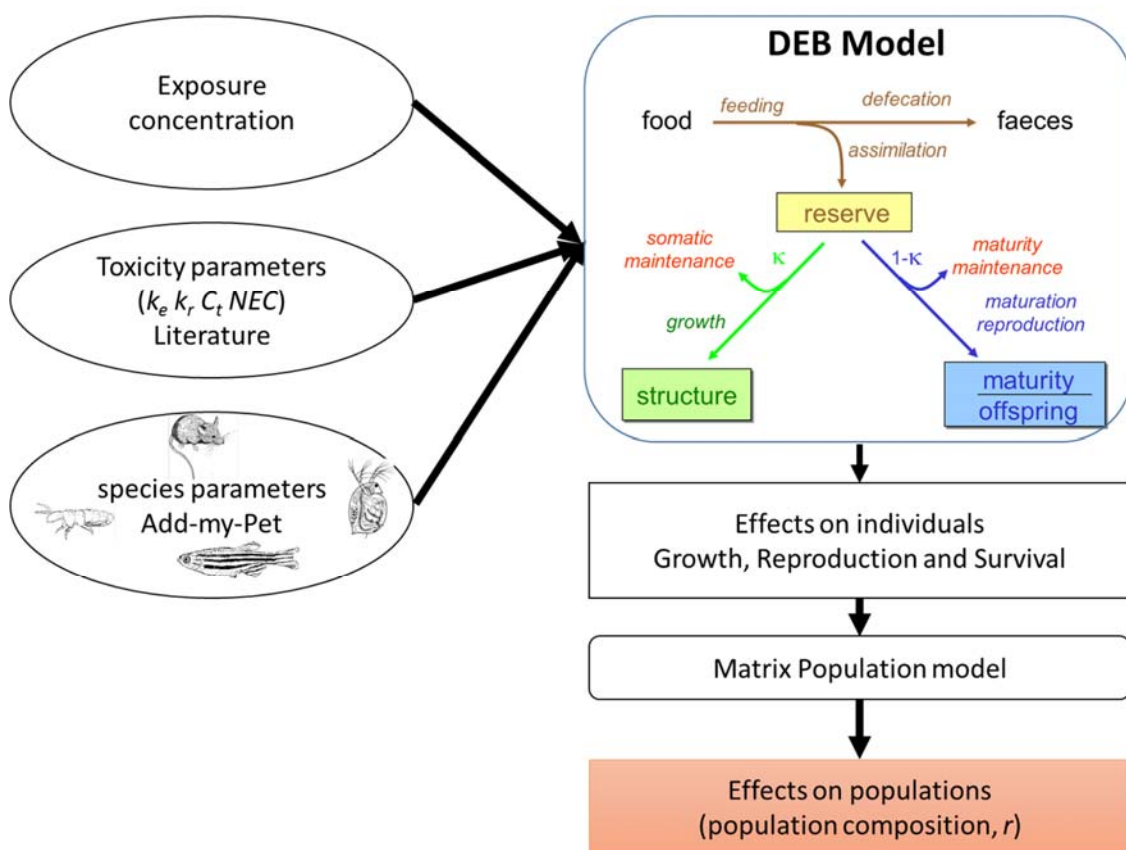
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Abstract

In ecological risk assessment of chemicals, hazard identification and hazard characterisation are most often based on ecotoxicological tests and expressed as summary statistics such as No Observed Effect Concentrations or Lethal Concentration values and No Effect Concentrations. Considerable research is currently ongoing to further improve methodologies to take into account toxicokinetic aspects in toxicological assessments, extrapolations of toxic effects observed on individuals to population effects and combined effects of multiple chemicals effects. In this context, the principles of the Dynamic Energy Budget (DEB), namely the conserved allocation of energy to different life-supporting processes in a wide variety of different species, have been applied successfully to the development of a number of DEB models. DEB models allow the incorporation of effects on growth, reproduction and survival within one consistent framework. This review aims to discuss the principles of the DEB theory together with available DEB models, databases available and applications in ecological risk assessment of chemicals for a wide range of species and taxa.

Future perspectives are also discussed with particular emphasis on ongoing research efforts to develop DEB models as open source tools to further support the research and regulatory community to integrate quantitative biology in ecotoxicological risk assessment.

44 Graphical Abstract



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48 Abbreviations

49 AmP: Add-my-Pet; DEB: Dynamic Energy Budgets; EFSA: European Food Safety
 50 Authority; LD_{50} : Lethal Dose for 50% of the individuals; LC_{50} : lethal concentration for
 51 50% of the individuals; NOEC: No Observed Effect Concentration; NEC: No Effect
 52 Concentration; EC: Effect Concentration; EC_x : concentration with x% effect; ERA:
 53 Ecological Risk Assessment; TK: toxico-kinetic; TD: toxico-dynamic.

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55 Highlights

- DEB theory is a framework for modelling time-specific lethal and sub-lethal effects.
- DEB models are promising tools for RA and have been applied to a variety of taxa.
- The Add-my-Pet database contains life cycle and DEB parameters for 857 species.
- Generic DEB models for RA are developed as open source tools as an EFSA project.

Keywords

Dynamic Energy Budget; ecological risk assessment; Add-my-pet; modelling; population dynamics

1 Introduction

Ecological risk assessment (ERA) of chemicals aims to characterise risks to the environment associated with chemical exposure combining an exposure and hazard dimension and to conclude on magnitude of effects that are deemed acceptable in relation to set protection goals (e.g. mortality). From a bird's eye view, frameworks for ERA often use tiered approaches which may depend on the aim of the assessment, the data available, and time-resources. For hazard identification and hazard characterisation, the first tier may use ecotoxicological endpoints from standardised laboratory experiments with aquatic and/or terrestrial species and at high tiers, results from semi-field to field trials. Using a first tier approach for hazard identification and hazard characterisation of regulated compounds (including pesticides and feed additives) assessments are often based on

summary statistics like the No-Observed-Effect-Concentration (NOEC), Lethal Dose (LD_{50}), Lethal Concentration for 50% of the exposed individuals (LC_{50}) or 50% Effect Concentrations on growth (or growth rate) and reproduction (or reproduction rate) (EC_{50}) for a specified exposure time. Environmental quality standards are then usually derived using the lowest available summary statistics for the NOEC LD_{50} , EC_{50} , applying an uncertainty factor (UF) to derive a predicted no-effect concentration (PNEC). The UF that is applied depends on data availability but in most cases it is the standard default value of 100-fold UF. This default value may be replaced by data driven UFs depending of data availability on taxa specific toxicity such as chemical specific adjustment factors (CSAFs) applied in the human health area (WHO, 2005).

Over the last decade, considerable research efforts have been put together to further improve risk assessment methodologies particularly to take into account mechanistic understanding of toxicity. In the human risk assessment area, the **Mode of Action** (MoA) framework has been developed by the US-EPA and WHO as ‘a biologically plausible sequence of key events leading to an observed effect supported by robust experimental observations and mechanistic data’. MoA describes in a logical framework key cytological and biochemical events that are both measurable and necessary to the observed effect. MoA does not imply full understanding of **Mechanism of Action** (MeA) which relates to a detailed molecular description of individual biochemical and physiological key events leading to a toxic effect (Boobis et al., 2006; Meek et al., 2014)). In toxicological terms, the MoA framework provides means to investigate toxico-kinetics (TK) and toxico-dynamic (TD) processes at different levels of biological organisation (organism, organ,

cellular and sub-cellular level). TK describes the processes leading to the internal concentrations of a chemical or its metabolites(s) through knowledge of absorption (A), distribution (D), metabolism (M) and excretion (E) (ADME). TD describes the processes that lead to the toxic effects of a chemical or its metabolites(s) once it has reached the organ(s) or tissue(s) (EFSA, 2014). In ERA, a number of MoA classifications have been developed and include: 1. Verhaar classification using five broad categories based on general toxicological responses: class 1. narcosis or baseline toxicity; class 2. less inert compounds class 3 unspecific reactivity, class 4. compounds and groups of compounds acting by specific mechanism, class 5.unknown mechanism, 2. the U.S. Environmental Protection Agency (US-EPA) assessment Tool for Evaluating Risk (ASTER) MoA, 3. the US-EPA Mode of Action and Toxicity (MOAtox) database providing a high degree of specificity based on fish behavioural responses or weight of evidence classification (Kienzler et al., 2017).

The related concept of **Adverse Outcome Pathway** (AOP) emerged from the field of ecotoxicology and has been defined as ‘a sequence of events from the exposure of an individual or population to a chemical substance through a final adverse (toxic) effect at the individual level (from a human health perspective) or population level (from an environmental perspective)’(Ankley et al., 2010). AOPs that have been investigated and depicted are available on the AOP Wiki tool (aopwiki.org). Recent reviews provide strategies, principles and best practices (Villeneuve et al., 2014a; Villeneuve et al., 2014b). The mapping of AOPs is a very active area of toxicological research and advances have been made to bring AOP together into networks. A recent review provided a description of an AOP network based on five reproductive and developmental toxicity-related AOPs for

fish and illustrations on how such AOP networks can inform the development and refinement of laboratory assays (Knapen et al., 2015). Recently, (Teeguarden et al., 2016a) have introduced the aggregate exposure pathway (AEP) as an intuitive framework to organize exposure data including ADME/TK data. The AEP framework supports, while making use of existing exposure models, the improvement of the generation, organization, interpretation, modelling and prediction of data from exposure sciences including ADME/TK information (Teeguarden et al., 2016b). In practice, the AEP also provides a holistic exposure counterpart to the AOP framework and a flexible tool to integrate the two frameworks together to apply risk-based, hazard-based, or exposure-based approaches in chemical risk assessment (Teeguarden et al., 2016a).

In the food safety area, EFSA recently published a review on « Modern methods for human hazard assessment of chemicals» which focused on mechanistic means to investigate TK and TD processes for human risk assessment of chemicals. These included *in vitro* systems to move towards the use of alternative approaches to animal testing, physiologically-based (PB) models (such as PB-TK and PB-TK-TD models), and computer models including (Quantitative) Structure Activity Relationship (Q)SAR systems), read across methods as well as OMICs technologies (transcriptomics, proteomics, and metabolomics) (EFSA, 2014). Consultation of EFSA experts and other international organisations identified important needs to develop open source platforms for PB-based models to further explore their applicability and integration in chemical risk assessment for single and multiple chemicals (EFSA, 2013; EFSA, 2014). Specifically, the models should be calibrated using specific case studies to illustrate the integration of exposure, TK information and toxicity

data, databases providing critical parameters to build these models (physico-chemical, physiological, toxicological) and bioinformatic tools/algorithms to analyse and integrate such data (EFSA, 2014).

In ERA, key empirical and mechanistic models have been developed over the last two decades for terrestrial and aquatic species such as physiologically-based TK models (PB-TK), physiologically-based TK-TD models (PB-TK-TD) (Grech et al.) and dynamic energy budget (DEB) models which are the focus of this review. Here, the principles of the DEB theory and standard DEB models are introduced together with the available databases providing life cycle parameters to the standard DEB model. DEB models to assess impact of chemicals and other stressors on organisms at the individual and population level are then discussed with examples from the literature. Ongoing and Future work to develop open source DEB models to support the ecotoxicological scientific community conclude.

2. DEB theory and DEB models: Fuelling the life cycle with energy and mass from individuals to populations

2.1. DEB theory and the standard DEB model

Historically, the DEB theory finds its origin in 1979 in an ecotoxicology laboratory in the Netherlands (Delft) investigating the toxicology of chemicals on daphnids and several species of fish. The main question raised during these experiments was how to incorporate growth and reproduction in a consistent quantitative framework that would apply to

different taxa? This was the starting point in the line of reasoning that kick started DEB theory.

The observation that growth curves of very different species like daphnia and fish are very similar in their appearance (typically characterised by Von Bertalanffy growth (Bertalanffy, 1938)), despite huge possible differences in the numbers along the axes, raises the question on the existence of underlying fundamental principles. The DEB theory deals with these underlying principles and describes how energy and mass from environmental resources are used over time to fuel the life cycle of an organism under physiological conditions (e.g. feeding, maintenance, growth, development and reproduction) into one consistent framework. Conservation of mass and energy as well as species specific stoichiometric constraints are also taken into account.

From the DEB theory, a number of families of related models have been derived with various levels of complexity. The complexity of the model (parameters and state variables) depends on the questions one is interested in and the availability and quality of data available. The simplest complete DEB model is the standard DEB model in which an organism consists of one structure and one reserve and feeds on one food source (see Figure 1) (Kooijman, 2010). The standard DEB model assumes that the shape of an organism from a particular species does not change during growth and that the life cycle is defined by three life stages: embryo, juvenile and adult.

figure 1 somewhere here

Figure 1 Schematic presentation of the standard DEB model

Boxes: state variables for the individual. Arrows: energy fluxes for the process specified by the arrow

Figure 1 highlights that in the standard DEB model food is taken up by the organism and is stored in reserves from which food is mobilized and used to grow, mature, reproduce and maintain the integrity of the system. The use of the mobilized flux follows the so called kappa-rule. The kappa-rule states that a fixed fraction of the available reserves is used for growth and somatic maintenance and the remaining part is used for development, maturity maintenance and reproduction. κ is assumed to be a constant over the lifetime of an individual, this assumption implies that growth and reproduction do not compete directly for resources. Embryos (which do not feed or reproduce) and juveniles (which feed but do not reproduce) use the available energy from reserves for the development of physiological systems and reproductive organs.

In each of these two branches priority is always given to maintenance: somatic maintenance the κ branch and maturity maintenance in the $(1 - \kappa)$ branch. If the rate of energy utilisation from the reserves is no longer sufficient to sustain the maintenance costs, there are several options depending on the species: the individual might die, it might exceptionally use energy from the reproduction buffer or if possible it might shrink/lose weight reducing the maintenance costs. As development stops at puberty, when a juvenile organism becomes adult, the energy is then reassigned to fuel reproduction, typically in the form of a reproduction buffer. When sufficient data are available and whenever needed, the standard DEB model can be extended to incorporate biological traits for specific taxa

214 or default values under data poor conditions. For example, when developing DEB models
215 for plants, it is essential to introduce more than one structure or primary producers would
216 need more than one reserve (Kooijman, 2010). Different biological traits can be included
217 in the standard DEB model as extensions, with conservation of the interpretation of
218 parameters and parameter values.

219 Elaborate descriptions of the background of DEB theory and the fundamental mathematical
220 equations can be found in (Kooijman, 2010; Kooijman et al., 2008; Lika et al., 2011a; Lika
221 et al., 2011b; Meer, 2006; Sousa et al., 2010).

222 **2.2 Linking the DEB parameters to standard life-cycle parameters**

223 The eight parameters that describe the standard DEB model represent the energetics of an
224 organism and cannot be observed directly but can be derived from standard life-cycle data
225 (VU-Theoretical-Biology, 2017) such as:

226

227 -Time to hatching

228 -Body length at birth

229 -Weight at birth

230 -Growth rate

231 -Physical length at puberty

232 -Age at puberty

233 -Weight at puberty

234 -Time to first reproduction

235 -Final body length

- Final body weight
- Max reproduction rate
- Lifespan

Such life-cycle parameters then feed into the DEB model from which the underlying DEB parameters are derived (Lika et al., 2014; Lika et al., 2011a; Lika et al., 2011b). The overall quality of the data and the size of the database determine the extent to which the DEB parameters can be derived (Jager and Zimmer, 2012).

When the same group of organisms is followed over time in the laboratory, the resulting data are not independent. The model usually predicts reproduction as a continuous rate (e.g., number of eggs per day) for which a discrete number of offspring, produced by one or more females in a time interval, are observed. In addition, growth and reproduction are graded endpoints, whereas survival is a quantal endpoint. Although these endpoints are not directly comparable, they do share information about the same underlying parameters.

Any model is a simplification of reality and specifically biological data always show variation which creates scatter in the data. Therefore in any practical application much attention is given to the optimization procedure of estimating the parameters e.g. (Lika et al., 2011b).

2.3 DEB models coupling toxico-kinetics and energetics at the individual level: DEB-TOX and DEB-Kiss

2.3.1 The DEB tox model

The DEBtox model constitutes an application of the DEB theory to understand toxic effects and was first developed to address incorporation of different endpoints as the results of ecotoxicological testing. The link between TK/metabolism and toxic effects was first introduced in 1984 by Kooijman and Metz (Kooijman and Metz, 1984) who designed a model that already had most of the characteristics of the current DEB model except for the reserve dynamics. Later on the approach was further refined by Kooijman, Bedaux and Jager and co-workers (Jager et al., 2004; Kooijman and Bedaux, 1996). The general approach was adopted by the OECD in the guidance document dealing with “current approaches in the statistical analysis of ecotoxicity data: a guidance to application” (OECD, 2006). The main difference with classical ERA is that in classical ERA summary statistics from laboratory studies in standard test species are used. These include EC_{50} for growth (or growth rate), EC_{50} for reproduction (or reproduction rate), LC_{50} for survival and NOEC for growth and/or reproduction for a fixed exposure time depending on the species. By definition, single time-point summary statistics do not take into account TK and TD processes.

The DEBtox approach takes into account TK and TD processes. In the environment, organisms get exposed to chemicals and the first step leading to a pharmacological or toxicological effect is uptake from the environment (external dose) by the organism either through soil, air, water or food. Two critical processes are then involved namely “what the body does to the chemical”: the TK, as the action of the body on the substance and “what the chemical does to the body”: the TD, as the action of the substance on the body

(Benfenati et al., 2017; Spurgeon et al., 2010). Therefore a kinetic module should be the starting point for any further steps. In practice, an elimination rate (TK) is derived from the observed time course of toxicity (TD). In this context, the elimination rate does not necessarily reflect the whole body elimination but the rate determining step in linking internal concentrations to effects (TD) (Zitko, 1979).

The toxicant, once inside the organism and above some threshold level, may have an effect on growth, reproduction and or survival. This leads to the interpretation that toxicants result in physiological/toxicological modes of action, that affect life cycle traits by influencing (at least) one of the processes identified by DEB theory, see also figure 1 (Álvarez et al., 2006):

- increasing maintenance costs
- decreasing the assimilation of energy from food
- increasing the energetic costs for growing new body tissue
- increasing the energetic costs for producing offspring
- posing a direct hazard to the developing embryo

Recently, Ashauer and Jager (Ashauer and Jager, 2018) have defined these parameters as “*physiological MoA :a distinct way in which a chemical interferes with the energy fluxes in an organism, and thereby affects life-history traits*” including maintenance, assimilation, growth costs, reproduction costs and hazard to embryo. Here, the term DEB Mode of Action (DEBMoA) is applied since physiological mode of action may also be interpreted

in terms of physiology and not strictly speaking in toxicological terms as “adverse” with regards to life cycle functions.

Three parameters are needed to describe the whole time-course of toxic effect (Kooijman and Bedaux, 1996):

- A time-independent toxicological threshold below which no effects occurs irrespective of exposure time the No Effect Concentration (NEC)), (as the incipient LC_0). The NEC usually expressed as an environmental concentration).
- A TK parameter (k_e) which describes when the equilibrium between internal and external concentration is set expressed in d^{-1} .
- A TD parameter that relates to the toxic potency of the compound; the killing rate (k_r) expressed in $(mol/l)^{-1}day^{-1}$ for survival and the tolerance concentration (C_t) for sub-lethal effects expressed in mol/l . The higher the killing rate and the lower the tolerance concentration the more potent the toxicity of a compound.

From an ERA point of view, the threshold concentration is the most important parameter (Baas et al., 2010a; Jager et al., 2006) and is also a more suitable metrics to compare species sensitivity or the toxicity of different compounds compared with EC_x or LC_{50} values (Baas and Kooijman, 2015; Jager et al., 2006). In fact EC_x or LC_x values can be calculated for any value of x for any point in time using a DEB model coupled to a TK/TD module. By

making use of the DEB framework all parameters can be extrapolated from one species to the next and ranges of biologically plausible values exist (Lika et al., 2014).

In all applications, integrated effects on growth and reproduction need to be translated to the underlying DEB parameters and mechanism (Lika et al., 2011a; Lika et al., 2011b). The overall quality of the data and the extensiveness of the dataset (body size over time, timing of spawning events, number of offspring, survival over time) determines to what extent this can be carried out. Still the mode of toxic action can be difficult to extract from available data (Jager et al., 2014a; Muller et al., 2010a). Another practical consideration is that the actual model parameters are calculated from their counterparts in the controls. So having a reliable control is crucial to interpret which of the parameter values are affected in order to derive the physiological mode of action.

With exposure above the threshold value toxic effects will develop over time, which is mathematically interpreted as a change in parameter values in the affected process, defining the DEBMoA. Each DEBMoA has specific consequences for the patterns of growth and reproduction over the life cycle (Álvarez et al., 2006).

The survival module of the model can be used as a stand-alone part of the modelling framework and consists of a scaled one-compartment model to describe uptake and elimination and a hazard model to describe survival. This basically leaves out all the energetics leading to a much simpler approach but it still gives a dynamic description of the toxicity process, allowing to deal with e.g. time-dependent exposures and growth dilution. In DEB theory the assumption is that death can be described by the hazard model,

contrary to the more frequently used LC_{50} where the underlying assumption is an Individual Threshold (IT). When this threshold is reached the individual will die. In the hazard model it is assumed that all species are equally sensitive and death is a chance process, whereas in the IT approach it is assumed that the most sensitive ones die first. This has far reaching consequences: if a cohort of individuals is exposed a second time to an LC_{50} concentration, the IT model predicts no mortality in the second exposure and the hazard model predicts again 50% mortality, like it was found in a dedicated experiment (Newman and McCloskey, 2000). See also the description of the so called GUTS framework for survival where an excellent description of the different approaches for survival is given and how the different approaches relate to one another (Jager et al., 2011) and how the models can be applied and extended (Ashauer et al., 2016; Ashauer et al., 2015).

2.3.2 .The DEBkiss model

The DEBkiss model has been introduced recently in the literature for the interpretation of ecotoxicological data. The DEBkiss model is similar to the historical Kooijman-Metz model (Jager et al., 2013b; Kooijman and Metz, 1984) both exclude the reserve dynamics so that metabolic memory is not included and predictions for species in conditions with lack of food become troublesome (see figure 2). In general terms, the reserve dynamics and the underlying mechanism is probably the most debated part of general DEB theory (Meer, 2006). Advantages of the DEBkiss approach lie in the derivation of simpler models in terms of number of state variables (Jager et al., 2013b). The loss of one or two state variables comes at the cost of biological realism and extrapolation potential since the DEBkiss model is more species and context specific compared with the standard DEB model. Nonetheless, the DEBkiss approach has been very useful in helping understand

effects over time under complex exposure situations (like repeated pulsed or mixtures). Moreover, if the kinetics of mobilising the reserves is fast and metabolic memory is not needed (e.g. organisms are fed *ad libitum* for an ecotoxicological test), the DEBkiss model can be applied as a simplified version of the standard DEB model, with a comparable interpretation of ecotoxicological test results (Jager et al., 2013b). A direct comparison between the two models showed similar predictions if toxic effects on individuals were extrapolated to effects on the intrinsic population growth rate (Jager and Klok, 2010b) with a slightly better extrapolation potential of the more elaborate model. Maturity of the organism (i.e. the switch to start reproduction) is also generally excluded in DEBkiss models however this can be included if needed.

Figure 2, somewhere here

Figure 2 Graphical representation of the DEBkiss model. Here all energetic costs for growth, maintenance and reproduction are taken up from food uptake without first being taken up as reserves.

Critically, as reserves are one of the cornerstones of standard DEB theory alongside exploiting mass and energy conservation, care has to be taken in the interpretation and comparison of different models derived by either DEBkiss or the standard DEB model. Parameters have different interpretations (though the same parameter abbreviations are used) depending on the framework and may impact on conclusions regarding hazard characterisation of a chemical or stressor.

2.4 DEB population modelling

Effects on individuals can be substantially different from effects on populations. For instance, comparable reductions in reproduction due to toxic stress at an individual level were demonstrated to lead to very large differences in effects at the population level (Beaudouin et al., 2015; Martin et al., 2012). Population level effects are considered to be an important aspect of ERA but are not (yet) often taken into account routinely (Forbes and Calow, 1999; Forbes et al., 2010). There is a general consensus that DEB-based modelling offers a first step towards population modelling since key features of an individual organism's life-cycle impacting on the population (growth, reproduction and survival) are captured within a consistent and well tested theoretical framework (Ananthasubramaniam et al., 2015; Bacher and Gangnery, 2006; Jager et al., 2014a). Currently, DEB modelling, with a growing database, historical data and experience of use, can also be applied as a predictive *in silico* tool allowing to perform informed extrapolations of toxic effects for untested concentrations and other environmental conditions, such as food limitation.

Under constant environmental conditions (and excluding intra- and interspecific interactions and density effects), populations grow following an exponential model, with an asymptotic population growth rate (r) (Billoir et al., 2007; Forbes et al., 2010). The influence of toxicants on life-history traits (survival and reproduction) can directly be expressed as a decrease in r . Even though it is clearly unrealistic to expect prolonged exponential growth in real populations, r reflects the inherent capacity of a population to adapt to adverse effects or bounce back from a drastic decline in numbers. Therefore, r can be considered a general fitness measure for the population (Forbes et al., 2010). Note that

the underlying implicit assumption here is that each new generation will have identical sensitivity. This is not necessarily the case, and sensitivity of later generations may be substantially different as demonstrated recently in multi-generation studies and such information may be accounted for in the population modelling, however, often not available even though highly relevant to ERA (Biron et al., 2012; Schultz et al., 2016).

In general, steps for the modelling of individuals to the population level include rules for interaction(s) between individuals and for the transport of resources in the environment. The simplest interaction rule for the standard DEB model is that individuals only interact via competition for resources. In the case of organisms that reproduce by division, the transition from the individual to the population is much simpler and a population of a few adult individuals may behave identically to that of many small ones if the sum of their masses matches. Here, the individual level is not critical but the population itself (Kooijman, 2010). This was used in Poggiale et al. (Poggiale et al., 2010), where population performance was directly linked to sub-individual physiology. There are various DEB based applications to extrapolate toxic effects on individuals to populations using different types of population models and these are either based on complete DEB models or simplified approaches (Alver et al., 2006; Ananthasubramaniam et al., 2015; Bacher and Gangnery, 2006; Beaudouin et al., 2015; Billoir et al., 2007; Biron et al., 2012; Jager and Klok, 2010a; Klanjscek et al., 2006; Kooijman et al., 1989; Martin et al., 2014; Martin et al., 2013; Martin et al., 2012; Nisbet et al., 2010).

3. Databases and Tools for DEB modelling

DEB modelling is applicable when the relevant variables can be generated such as the No Effect Concentration (NEC) which constitutes a model parameter that can be interpreted and applied in ERA. In other cases, dynamic simulation studies might be required and the DEB model might have to be coupled to fate and transport models or parameters controlling offspring production integrated into population level models (see above population models) (Kooijman, 2012). Figure 3 illustrates a generic DEB population modelling approach under which species and compound properties as well as toxic effects feed into the standard DEB model for individuals as DEB-modes of action (such as an effect on assimilation) and output parameters modulated by the toxicant. The general output of the population DEB model is given as the survival probability of the individuals and the impact on reproduction.

Figure 3 somewhere here

Figure 3 Schematic representation of DEB population modelling. The ellipses are input data, the boxes the different models and the rounded boxes model output.

3.1 Add My Pet: A Database for DEB modelling

DEB parameters describing the energetics of species cannot be derived directly from observations on species but are estimated using the underlying life history parameters (as was described in section 2) and these together define the underlying DEB parameters.

Information and quantitative data on the eco-physiology and life-history traits of different species can be collected from several major databases: Add-my-Pet, Animal Diversity Web, Encyclopedia of Earth and Fish Base (Kooijman et al., 2017).

The Add-my-Pet (AmP) database summarises the underlying energetics that together capture life history data, to derive DEB parameters. AmP is a pan European initiative and is extensively documented using collaborative online media wiki powered software. For this reason, AmP is the natural information base for supporting ERA of single and multiple chemicals. Other databases (Animal Diversity Web, Encyclopedia of Earth and Fish Base) are typically used for life cycle data, which are then used to generate DEB parameters for more species to populate the AmP database.

AmP is an initiative, which started in 2009, in the context of much wider aims than ERA: find the simplest organisation principles for metabolism upon which all life is based and understand taxon-specific patterns as variations on this common theme. It turned out that a number of extensions on the standard DEB model were needed to capture specific life-history of various groups of species. The overall model can therefore vary from taxa to taxa but it is also possible to use different extensions of the standard model for a single species depending on the level of refinements one wants the model to achieve. This approach can be followed without any loss of consistency and parameter values can be compared for different species. Some examples of model extensions are relaxing the assumption of constant shape whereby changes in shape allow metabolism to accelerate for part of the life-cycle. Or including extra-life stages (for instance weaning for mammals), reversing the order of life-stages (adults come before embryos for insects), and choosing different modes

of reproduction (foetal or egg development). Parameters values for the different species remain comparable for the different variations.

The AmP collection contains data for 871 species (AmP, 2017/06/12) from all of the large phyla excluding sponges (cnidaria) (see figure 4). Furthermore, there are species belonging to each chordate order, with the exception of some deep water ray finned fish and marsupial moles. Finally, there are species from all of the primate families. The standard DEB model assuming either egg or foetal development captures the life-history of about two thirds of the taxa present in the collection quite well.

Figure 4, somewhere here

Figure 4 Overview of species in Add-my-Pet and the number of species included in Add my-pet over time (06/12/2017)

3.2 Ecotoxicological Databases and QSAR models

For effects on survival, DEB toxicity parameters can be derived if LC_{50} values are available at different points in time or by making use of QSARs (Baas et al., 2015; Jager and Kooijman, 2009).

Most available databases report single time point toxicity data, which have yet limited applications in process-based approaches or TK-TD modelling. The ECOTOX database, hosted by the United States Environmental Protection Agency (US-EPA, 2013) is currently the most complete database existing for which a plethora of toxicity data published in the

scientific literature have been gathered and summarised, including some LC_{50} data for multiple points in time. The US-EPA ECOTOX database has been extensively used for the determination of DEB parameters for survival for pesticides using multiple points in time which are present for a limited number of substances (Baas et al., 2009a; Baas et al., 2016a). For sub-lethal toxicity, the time course of toxic effects is not straightforward and parameters have not been derived from EC_{50} data over time (Baas et al., 2010a; Jager et al., 2006).

The Pesticide Property Database (PPDB) is a comprehensive relational database of pesticide chemical identity, physicochemical, human health and ecotoxicological data. It contains data on all pesticides that are allowed in the EU and contains data on 1150 pesticides, 700 metabolites and some 100 related compounds. It has been developed by the Agriculture & Environment Research Unit (AERU) at the University of Hertfordshire for a variety of end users to support risk assessments and risk management (Lewis et al., 2016). The database is fed with pesticide properties based on the monographs produced as part of the EU review process published by EFSA. Where EFSA documents are not available, alternative sources are used. This implies that the vast majority of the data is well documented and measured according to the latest ISO regulations.

4. Applications of DEB models in ERA

The potential combinations of species and chemicals that may be present in a particular ecosystem is vast and performing ERA represents a challenge because of such complexity and the limited quantitative knowledge on a wide range of taxa specific traits. Most often, ERA is based on inter-species extrapolations where default uncertainty factors are applied

to account for lack of knowledge on inter-species TK and TD and allow site specific ERA. In general terms, extrapolation operates (i) from individual to population (section 4.1), (ii) from species to species (section 4.4), (iii) from chemical to chemical (particularly for compounds that are structurally related) (section 4.3), (iv) from a single chemical to mixtures of chemicals (section 4.2). Since data for sub-lethal effects are often scarce (see section 3), (v) extrapolation are from lethal effects sub-lethal effects are most common. The DEB theory allows to perform extrapolations (i) to (iv) but to our knowledge, the derivation of sub-lethal effects from lethal effects has not been explored yet. However, options are available for such extrapolations to be performed using TK parameters that are derived from time course toxicity studies for lethal and sub-lethal effects using DEB theory and other frameworks for extrapolations (Hendriks and Heikens, 2001; Hendriks et al., 2001). Specifically, the DEB theory provides a means to quantify parameters related to how individuals progress their way through life and how stressors affect specific parameter values. Species properties (taxa-specific traits) are combined with physical (conservation) and chemical (stoichiometry) constraints so that all measurable endpoints such as growth and feeding are interlinked “there is 'no free lunch” (Jager et al., 2013a) and the response/sensitivity of an organism is deeply linked to the metabolic evolution of the organism survival in its specific environment. Finally, DEB models also allow the incorporation of effects resulting from exposure to non-chemical stressors such as food availability, temperature, salinity, parasites, etc.

In this context, a concise overview of taxa-specific and chemical specific DEB models is provided below. For this purpose, an extensive literature search was performed in a number

of databases (SCOPUS, Faculty of 1000, ZETOC, Elsevier, Medline/PubMed, Springer link, Taylor and Francis Crossref, GALE, AGRIS, Wiley, AIP, JSTOR, Picarta, Web of Knowledge and Web of science) to report two board categories of case studies:

- Research investigating effects of chemicals on taxa-specific lethal and sub-lethal endpoints for single and multiple chemicals, with a focus on the availability of TK and TD parameters that could serve as input for population dynamics modelling based on DEB theory. The separation of TK and TD provides a quantitative understanding of TK parameters over time linked to TD and compared with controls);
- Case studies providing means to extrapolate individual effects on single species to a population.

Key words included in the extensive literature search included:

- DEB
- Dynamic Energy Budget
- Mixtures
- Ecotoxicology
- Modelling
- Mortality
- Growth
- Reproduction

- Population Dynamics

- Individual based modelling

Assessment criteria

- Consistency
- Method, full description, source code available?
- Biological relevance
- Study design, was the model applied to measured data and how
- Parameterization of the model, do the parameters relate to biological traits?
- Biological relevance, do the parameters relate to biological traits
- Application to bio-assays

The number of papers extracted from the extensive are summarised in table 1.

Application	Nr of papers (after first selection)	Nr of relevant papers (after final selection)
DEB in ecotoxicology	27	18
DEB in mixtures	13	7
DEB in population dynamics	36	15

Table 1 Summary of results of the literature survey

The sections below provide summary tables for taxa specific DEB models and applications.

4.1 Taxa-specific DEB-based approaches to model toxico-kinetics and toxico-dynamics of chemicals

Taxa-specific DEB based approaches to model TK and TD impact of chemicals are given in table 2 and illustrates applications to a wide variety of aquatic taxa/species and shows limited data for terrestrial organisms. The diversity of taxa that have been modelled using these DEB approaches ranges from annelid and nematode worms, arthropods, mussels, daphnia and fish, however, the chemical space covered is still rather specific with most of the models developed on metals, pesticides and a few contaminants.

Phylum	Species	Stressor (s)	DEB Model	Reference
<i>Annelida</i>	<i>Dendrobaena octaedra</i>	Copper	DEBkiss	(Jager and Klok, 2010b)
<i>Annelida</i>	<i>Dendrobaena octaedra</i>	Copper	DEBtox	(Jager and Klok, 2010b)
<i>Annelida</i>	<i>Dendrobaena octaedra</i>	Copper	DEB	(Jager and Klok, 2010b)
<i>Arthropoda</i>	<i>Chironomus riparius</i>	Methiocarb	DEBMatrix population	(Lopes et al., 2005)
<i>Bacteria</i>	<i>Pseudomonas aeruginosa</i>	Cadmium	DEB hazard	(Klanjscek et al., 2012)

<i>Chordata</i>	<i>Danio rerio</i>	Uranium	DEB	(Augustine et al., 2012)
<i>Copepoda</i> (arctic)	<i>Calanus glacialis</i> and <i>Calanus finmarchicus</i>	PAHs	DEB	(Klok et al., 2012)
<i>Crustacea</i>	<i>Daphnia magna</i>	Cadmium	DEB Matrix population	(Billoir et al., 2007)
<i>Crustacea</i>	<i>Daphnia magna</i>	Uranium	DEBMatrix population	(Biron et al., 2012)
<i>Crustacea</i>	<i>Daphnia magna</i>	Fluoranthene	DEBkiss	(Jager and Zimmer, 2012)
<i>Crustacea</i>	<i>Daphnia magna</i>	3,4-dichloroanniline	DEB IBM	(Martin et al., 2012)
<i>Mollusca</i>	<i>Mytilus galloprovincialis</i>	ZnO nanoparticles	DEB	(Muller et al., 2014)
<i>Nematoda</i>	<i>Acroboloides nanus</i>	Pentachlorobenzene	DEB	(Álvarez et al., 2006)
<i>Nematoda</i>	<i>Acroboloides nanus</i>	Carbendazim	DEB	(Álvarez et al., 2006)

<i>Nematoda</i>	<i>Acrobelloides nanus</i>	Cadmium	DEB	(Álvarez et al., 2006)
<i>Nematoda</i>	<i>Caenorhabditis elegans</i>	Uranium	DEB	(Goussen et al., 2015)
<i>Nematoda</i>	<i>Caenorhabditis elegans</i>	Aldicarb	DEB	(Wren et al., 2011)
<i>Various</i>	<i>Various</i> (mussels, oysters, earthworms, water fleas and zebrafish)	Various (mercury, copper, chlorophenols, toluene, PAHs, tetradifon, pyridine)	DEB	(Muller et al., 2010a)
<i>Various</i>	<i>Various</i> (mussels, oysters, fish, water fleas)	Pesticides (carbofuran, carbaryl, Chlorpyrifos, Malathion)	DEB	(Baas and Kooijman, 2015)

Table 2 Overview of Taxa-specific DEB models available in the literature including model type (matrix population models, Individual based population models, hazard indicators only survival).

4.2 Modelling toxico-kinetics and toxico-dynamics of multiple chemicals using DEB

modelling

DEB models provide useful tools to model the combined toxicity of multiple chemicals. This specific application of DEB models was recently discussed as part of EFSA 's colloquium on "Harmonisation of human and ecological risk assessment of combined exposure to multiple chemicals" (EFSA, 2015). DEB based models have been developed for the interpretation and prediction of combined toxicity of chemical mixtures providing means to improve extrapolation potential. As with single toxicants, the temporal dynamics of combined effects induced by a chemical mixture on endpoints like survival or growth are not quantifiable using data from single time-point dose-response experiments. DEB models are intrinsically "biology based" and are essential for developing explicit hypothesis on mixture effects using dose addition as the default assumption or analysing evidence for interaction that may increase (synergy) or decrease toxicity (antagonism) (Baas et al., 2010).

In practice, a distinction can be made between DEB models for survival and DEB models for sub-lethal effects that usually also include effects on survival. Models investigating mixture effects on survival have been first developed for binary mixtures as component-based approaches (Baas et al., 2007) and were subsequently further developed to model effects of more complex mixtures with comparable constituents (Baas et al., 2009a; Baas et al., 2010b). Further development of DEB models then focused on actual complex environmental mixtures with up to 100 different constituents (including metals, pesticides, salts, nutrients, PAHs) (Baas et al., 2009b). For each model, predictions were compared

with available data. Models investigating sub-lethal mixture effects were first developed from binary mixtures with similar mode of action (2 PAHs) (Jager et al., 2010). These have been now generalised to binary mixtures for mixtures with a different modes of action (Jager et al., 2014b; Margerit et al., 2016) and such a generic approach is illustrated in in Figure 5.

Figure 5, somewhere here

Figure 5. Generic approach for modelling combined effects of chemical mixtures within the framework of DEB theory.

In principle, every chemical entity is characterised with its own TK and toxicity (TD) which may affect one or more DEB parameters. This is translated in the general DEB model to an effect on life-cycle traits such as body size (growth), reproduction and survival. Note that some interactions may take place physiologically as metabolic processes are often ruled by feedback loops affecting on growth and reproduction. Synergistic effects may occur under food limitation and exposure to toxicants thereby affecting maintenance and somatic growth, as they compete for the same allocated reserves (Jager et al., 2014b). In addition, body size determines feeding rate which feeds back to body size and body size in itself affects TK and the initiation and rate of reproduction. A chemical in a mixture producing adverse effects on growth of the exposed organisms may affect the TK of its neighbour mixture components and their effects on reproduction. A list of DEB based applications investigating combined toxicity of mixtures is given in Table 3.

Phylum	Species	Stressor (s)	DEB Model	Reference
Arthropoda	<i>Tribolium castaneum</i>	PAH	DEB mixture survival	(Baas et al., 2010b)
Arthropoda	<i>Folsomia candida</i>	Copper, Cadmium, Lead, Zinc	DEB mixture survival	(Baas et al., 2007)
Chordata	<i>Pimephales promelas</i>	Narcotics	DEB mixtures survival	(Baas et al., 2009a)
Crustacea	<i>Daphnia magna</i>	Mixture of toxicants	DEB mixtures survival	(Baas et al., 2009b)
Crustacea	<i>Daphnia magna</i>	Mixture of toxicants	DEB mixtures survival	(Baas et al., 2016b)
Crustacea	<i>Daphnia magna</i>	Binary mixture PAHs	DEB (mixture)	(Jager et al., 2010)
Mollusca	<i>Mytilus gallopro-</i>	Produced water	DEB	(Muller et al., 2010b)

	<i>vincialis</i> and <i>M. californianus</i>			
<i>Nematoda</i>	<i>Caenorhabditis elegans</i>	Cadmium Fluoranthene	DEBkiss mixture	(Jager et al., 2014b)
<i>Nematoda</i>	<i>Caenorhabditis elegans</i>	Uranium Cadmium	DEB mixture	(Margerit et al., 2015)

Table 3 Applications of DEB theory for modelling combined toxicity of chemical mixtures

4.3. Using DEB models for read across between species and chemical and natural stressors

Several DEB based publications demonstrated that good results in toxicity predictions for compounds with no experimental data available or for inter-species extrapolation in data-sparse conditions. This has been illustrated for a wide range of chemicals including metals, narcotics and various kinds of pesticides as well as impact of food limitation or temperature stress both on an individual and on a population level.

The DEBtox approach, particularly in the context of exposure chemical mixtures, is often challenged for requiring a ‘substantially higher data demand’ compared with standard approaches e.g. (Backhaus et al., 2013). This holds true for the characterisation of LC_x or EC_x values for mixtures based on fixed time-points as well for more elaborate experimental designs often lacking experimental data and requiring simplification of models (Jager et al., 2014a). However, the DEB modelling approach has an important asset providing a quantitative tool to test mixture toxicity for any x value in LC_x or EC_x (including zero) without the need to assess 50% effect level for random time point which may vary widely

across species. Most often, environmental risk assessors would then need to apply a safety factor as 50% of effect may be considered too high and not protective enough for the taxa. If the standard mixture models are applied to assessments other than the fixed time 50% effect level, they then become substantially more data intensive compared with the DEB-based approach. In addition, a successful approach has been developed to predict combined toxicity of a real life complex environmental mixture based on the TK-TD based DEB approach, readily available data combined with read across and QSAR applications (Baas et al., 2009b). In this case, standard methods to model mixture toxicity namely Concentration addition (CA) (Hewlett and Plackett, 1959) and Independent action (IA) (Bliss, 1939) both failed to make reliable predictions for the complex environmental mixture.

Finally, DEB models do not have the flaw of a single time point LC_{50} 48 hr which may need to be extrapolated to different exposure time. This also holds true for the extrapolation between mixture exposure expressed as toxic units to the effect size (i.e. here percentage of effect) (Baas et al., 2016b). Table 4 gives an overview of this application of DEB theory, including effects of temperature and food limitation.

Phylum	Species	Stressor (s)	DEB Model	Reference
Chordata	<i>Merluccius merluccius</i>	PCB accumulation	DEB	(Bodiguel et al., 2009)
Chordata	<i>Danio rerio</i>	Population growth	DEB IBM	(Beaudouin et al., 2015)

<i>Copepoda</i>	<i>Calanus sinicus</i>	Temperature	DEBkiss	(Jager et al., 2015)
<i>Crustacea</i>	<i>Daphnia magna</i>	Food limitation	Matrix Simplified DEB	(Nisbet et al., 2010)
<i>Crustacea</i>	<i>Daphnia magna</i>	Pesticide mixtures	DEB mixture survival	(Baas et al., 2016b)
<i>Crustacea</i>	<i>Daphnia magna</i>	Pesticide mixtures	DEB mixture survival	(Baas et al., 2009b)
<i>Mollusca</i>	<i>Crassostrea gigas</i>	Harvesting oysters	DEB IBM	(Bacher and Gangnery, 2006)
<i>Mollusca</i>	<i>Lymnea stagnalis</i>	Food limitation	DEB	(Zimmer et al., 2012)
<i>Mollusca</i>	<i>Lymnea stagnalis</i>	Food limitation	DEBkiss	(Jager et al., 2013b)
<i>Mollusca</i>	<i>Macoma Balthica</i>	population dynamics	Lotka DEB	(Kooi and van der Meer, 2010)

Table 4 The use of DEB theory in data sparse conditions and for non-standard stressors like temperature or food limitation

4.4 Using DEB models to quantify interspecies differences in toxico-kinetics and toxico-dynamics of chemicals

Recently, DEB-based models have been developed to quantify interspecies differences in TK and TD and are summarised in table 5. For example, chronic time-course toxicity bioassays (10-day) have been performed in three bee species (honey bee, solitary bee and

bumble bee) for six chemicals and six mixtures and survival DEB-models were fitted to the experimental data to determine the elimination and killing rate of the individual compounds and mixtures. To date, these results provided the first time-course chronic datasets and inter species comparison for three bee species (Hesketh et al., 2017; Hesketh et al., 2016; Robinson et al., 2017).

Phylum	Species	Stressor (s)	DEB Model	Reference
<i>Arthropoda</i>	<i>Apidea</i>	Pesticides/metals	DEB survival	(Hesketh et al., 2016)
<i>Arthropoda</i>	<i>Apis mellifera</i> , <i>Bombus terrestris</i> , <i>Osmia bicornis</i>	Pesticides/metals	DEB survival	(Hesketh et al., 2017)
<i>various</i>	<i>Various</i>	narcotics	DEB survival	(Baas et al., 2015)
<i>various</i>	<i>Various</i>	pesticides	DEB survival	(Baas and Kooijman, 2015)

Table 5. DEB-based models investigating interspecies differences in toxico-kinetics and toxico-dynamics

5. Future directions and conclusions

This review provides an account of the DEB theory and applicability of DEB models to assess chemical toxicity on individuals and population dynamics of aquatic and terrestrial organisms. A key component of the approach is the separation of TK and TD processes, which provides (1) elimination rate as a key TK parameter, (2) time-independent toxicity parameters describing toxic effects for different endpoints and integrating them within one consistent framework using databases such as add my pet providing parameters for the standard DEB model. As a consequence, DEB models also provide a tool to quantify interspecies differences in TK and TD processes thus providing a basis for predictive modelling across taxa and chemical space.

In order to further enhance the applicability of generic DEB models for the modelling of population dynamics in terrestrial and aquatic organisms, a collaborative project between EFSA (Italy), the Centre for Ecology and Hydrology (UK), the High North Research Centre for Climate and the Environment (Norway) and Terraprima (Portugal) is exploring the development of open source DEB tools in R and their Applications in ERA for modelling toxicity of single and multiple chemicals at the individual and population level. This project further support the application of biologically-based models in ERA including PB-TK models as review elsewhere (Gresh et al., 2016).

Further work is recommended in this area to further support the application of biologically-based models in ERA including: 1. Development of open source databases providing *taxa specific parameters* (physiological parameters, molecular information on taxa specific

traits (e.g. receptor sequences, adverse outcome pathways etc..) and *chemical specific parameters* (physico-chemical properties, toxicity and TK parameters etc..). 2. Design of toxicity studies should be designed to provide an understanding of both TK and TD dimension to provide time-independent toxicological threshold, elimination rate of the compound and potency information on the compound. Examples of such study designs include the recent interspecies comparison studies in honey bees, solitary bees and bumble bees to investigate chronic toxicity (10 day) of pesticides and contaminants (single and mixtures).

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Disclaimer

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